ABSTRACT
Human infections with *Trichostrongylus* species have been reported in most parts of Iran. The aim of this study was the identification, molecular characterization and phylogenetic analysis of human *Trichostrongylus* species based on ITS2 region of ribosomal DNA from Guilan Province, northern Iran. Stool samples were collected from rural inhabitants and examined by formalin-ether concentration and agar plate culture techniques. After anthelmintic treatment, male adult worms were collected from five infected cases. Genomic DNA was extracted from one male worm of each species in every treated individual and one filariform larva isolated from each case. PCR amplification of ITS2-rDNA region was performed and the products were sequenced. Among 1508 individuals, 46 (3.05%) were found infected with *Trichostrongylus* species using parasitological methods. Male worms of *T. colubriformis, T. vitrinus* and *T. longispicularis* were expelled from five patients after treatment. Out of 41 filariform larvae, 40 were *T. colubriformis,* and the other one was *T. axei*. Phylogenetic analysis showed that each species was placed together with reference sequences submitted to GenBank database. Intra-species similarity for all species obtained in the current study was 100%. *T. colubriformis* was found to be probably the most common species in this region of Iran. For the first time, the authors of the present study report the occurrence of natural human infection by *T. longispicularis* in the world. Therefore, the number of *Trichostrongylus* species infecting human in Iran now increased to ten.
Keywords: *Trichostrongylus*; human; PCR; ITS2-rDNA region; phylogenetic analysis, Guilan; Iran.